WHAT IS CLAIMED IS:

1. A method of selecting a set of tag nucleic acids with minimal cross hybridization to a nucleic acid, said method comprising providing a list of tag nucleic acids, and excluding nucleic acids from the list of tag nucleic acids which cross hybridize to a single complementary nucleic acid under stringent conditions, thereby providing a set of selected tag nucleic acids with minimal cross hybridization to the nucleic acid.

2. The method of claim 1, wherein the method of selecting tag nucleic acids further comprises:

selecting a first tag nucleic acid from the list of tag nucleic acids;

selecting a second tag nucleic acid from the list of tag nucleic acids;

comparing the sequence of the first tag nucleic acid to the sequence of the second tag nucleic acid; and,

determining that the second tag nucleic acid hybridizes to the complement of the first tag nucleic acid with a selected thermal binding stability, thereby excluding the second nucleic acid from the selected set of nucleic acid tags.

3. The method of claim 2, wherein the method comprises rejecting or selecting each tag in the list of tags in order.

4. The method of claim 2, wherein tags are not selected if they have more than 8 contiguous nucleotides in common with any previous tag.

5. The method of claim 2, wherein the method comprises rejecting or selecting tags in complementary pairs, wherein each selected tag has a complementary selected tag.

6. The method of claim 1, wherein the method further comprises selecting a thermal binding stability for the tags, and excluding all tag nucleic acids from the list of tag nucleic acids which do not have the selected thermal binding stability.

7. The method of claim 6, wherein the thermal binding stability is selected by specifying a ratio of G+C to A+T nucleotides for the tag nucleic acids, and specifying a length for the tag nucleic acids.

8. The method of claim 1, wherein the method further comprises excluding tags which contain self-complementary regions from the list of tags.

9. The method of claim 6, wherein the regions of self complementarity are greater than 4 nucleotides in length.

10. The method of claim 1, wherein the tags are between 15 and 30 nucleotides in length.

11. The method of claim 1, wherein the tags are between 10 and 100 nucleotides in length.

12. The method of claim 1, wherein the tags are 20 nucleotides in length.

13. The method of claim 1, wherein the method further comprises selecting a complementary probe nucleic acid for tags in the selected tag set, wherein each tag sequence is complementary to one probe sequence, and the thermal binding stability between each tag and each complementary probe is substantially similar.

14. The method of claim 13, wherein all of the tags have the same length and the same GC to AT ratio.

15. The method of claim 1, wherein the method further comprises selecting a constant region subsequence shared by all tag nucleic acids, thereby determining the nucleotide position of variable nucleotides in the tags.

16. The method of claim 15, wherein the method further comprises providing a set of probe nucleic acids by determining the complement to each variable nucleotide in each tag nucleic acid, and selecting a probe comprising a corresponding complementary nucleotide for each nucleotide in the variable tag sequence, which probe does not hybridize to the constant region of the tag nucleic acid, thereby providing a selected set of probes.

17. The method of claim 1, wherein the method further comprises removing tag nucleic acids which have fewer than two nucleotide differences when aligned for maximal sequence correspondence.

18. The method of claim 17, wherein:

the total number of nucleotides in each of the selected sets is identical;

the number of G+C nucleotides in each tag in the selected set is identical; and,

the overall number of A+G nucleotides in each of the variable regions of the tags is even.

19. The method of claim 1, wherein the method further comprises removing tag nucleic acids which have fewer than 5 nucleotide differences when aligned for maximal sequence correspondence.

20. The method of claim 1, wherein tags which contain 4 contiguous nucleotides selected from the group consisting of 4 X residues, 4 Y residues and 4 Z residues, are eliminated from the tag set, wherein X is selected from the group consisting of G and C, Y is selected from the group consisting of G and A, and Z is selected from the group consisting of A and T.

21. A composition comprising a set of tag nucleic acids, which set of tag nucleic acids comprises a plurality of tag nucleic acids, which tag nucleic acids comprise a variable region;

which variable region for each tag nucleic acid in the set of tag nucleic acids has the same T_m, the same G+C to A+T ratio, the same length and does not cross-hybridize to a probe nucleic acid; and,

wherein the tag nucleic acids in the set of tag nucleic acids cannot be aligned with less than two differences between any two of the tag nucleic acids in the set of tag nucleic acids.

22. The composition of claim 21, wherein the tags comprise a constant region.

23. The composition of claim 21, wherein the variable region of each of the tag nucleic acids in the tag set comprises less than two C nucleotides.

24. The composition of set of claim 21, wherein the variable region of the tag nucleic acids from the set of tag nucleic acids comprises an even number of A+G nucleotides.

25. A method of labeling a composition, comprising associating a tag nucleic acid with the composition, wherein the tag nucleic acid is selected from a group of tag nucleic acids which do not cross-hybridize and which have a substantially similar T_m.

26. The method of claim 25, further comprising detection of the tag nucleic acid.

27. The method of claim 25, further comprising detection of the tag nucleic acid by labeling the nucleic acid and hybridizing the nucleic acid to a solid substrate, which substrate comprises an array of probe nucleic acids selected to hybridize to the group of tag nucleic acids.

28. The method of claim 25, further comprising amplification of the tag nucleic acids, thereby providing amplified tag nucleic acids and detection of the amplified

tag nucleic acids by hybridization to an array of probes complementary to the tag nucleic acids.

29. The method of claim 28, wherein the tag nucleic acids are amplified using the polymerase chain reaction.

30. The method of claim 28, wherein the amplified tag nucleic acids are labeled with a fluorescent label.

31. A method of pre-selecting experimental probes in an oligonucleotide probe array, wherein the probes have substantially uniform hybridization properties and do not cross hybridize, comprising:

selecting a ratio of G+C to A+T nucleotides shared by the experimental probes in the array;

determining all possible 4 nucleotide subsequences for variable nucleic acids in the probes of the array; and

excluding all probes from the array which contain prohibited 4 nucleotide subsequences, wherein 4 nucleotide subsequences are prohibited when the nucleotide subsequences are selected from the group consisting of self-complementary probes, A_4 probes, T_4 probes, $[G,C]_4$ probes, and probes complementary to constant region subsequences.

32. The method of claim 31, wherein the method further comprises

selecting a length for the probes in the array, thereby providing selected length probes;

selecting a constant region subsequence shared by all selected length probes in the array, thereby determining the nucleotide position of variable nucleic acids in the probes of the array; and

providing that the overall number of A+G nucleotides in the probes of the array is even.

33. The method of claim 31, wherein the method further comprises selecting control probes for addition to the array.

34. A method of detecting a plurality of nucleic acids in a sample, comprising

(i) providing an array of experimental oligonucleotide probes, which probes do not cross hybridize under stringent conditions, wherein the ratio of G+C bases in each probe is substantially identical;

wherein the probes of the array are arranged into probe sets in which each probe set comprises a homogeneous population of oligonucleotide probes;

(ii) hybridizing said array of oligonucleotides to the sample under stringent hybridization conditions; and

(iii) detecting hybridization of the nucleic acids to the array of oligonucleotide probes.

35. The method of claim 34, wherein the probes of the array specifically hybridize to at least one nucleic acid in the sample.

36. The method of claim 34, wherein the nucleic acids comprise tag sequences, which tag sequences bind to the probes of the array.

37. An array of oligonucleotide probes comprising a plurality of experimental oligonucleotide probe sets attached to a solid substrate, wherein

each experimental oligonucleotide probe set in the array hybridizes to a different target nucleic acid under stringent hybridization conditions;

each oligonucleotide probe in the probe sets of the array comprises a variable region; and wherein

the nucleic acid probes do not cross-hybridize in the array.

38. The array of claim 37, wherein each probe set in the array a constant region, wherein the variable region does not cross hybridize with the constant region under stringent hybridization conditions.

39. The array of claim 37, wherein each probe set in the array differs from every other probe set in the array by the arrangement of at least two nucleotides in the probes of the probe set.

40. The array of claim 37, wherein the ratio of G+C bases in each probe for each experimental probe set is substantially identical.

41. The array of claim 37, wherein the array comprises a plurality of probe sets selected from the output group of probes produced by running tags.ccp.

42. The array of claim 37, wherein the array further comprises a nucleic acid bound to a probe in the array.

43. The array of claim 37, wherein the array further comprises control probes.

44. A method of detecting a target nucleic acid comprising providing a population of nucleic acids to an array of oligonucleotide probes and monitoring hybridization of the test nucleic acids to the probes in the array, wherein the array of oligonucleotide probes comprises a plurality of experimental oligonucleotide probe sets attached to a solid substrate, wherein

each experimental oligonucleotide probe set in the array hybridizes to a different target nucleic acid under stringent hybridization conditions;

each oligonucleotide probe in the probe sets of the array comprises variable region; and wherein

the nucleic acid probes do not cross-hybridize in the array.

45. The method of claim 44, wherein the probes of the array comprise a constant region, wherein the variable region does not cross hybridize with the constant region under stringent hybridization conditions.

46. The method of claim 44, wherein the array comprises a control probe, and wherein the method further comprises hybridizing a nucleic acid complementary to the control probe to the array.

47. A plurality of recombinant cells comprising tag nucleic acids selected from a set of tag nucleic acids, which set of tag nucleic acids comprises a plurality of tag nucleic acids, which tag nucleic acids comprise a variable region;

which variable region for each tag nucleic acid in the set of tag nucleic acids has the same T_m, the same G+C to A+T ratio, the same length and does not cross-hybridize; and,

wherein the tag nucleic acids in the set of tag nucleic acids cannot be aligned with less than two differences between any two of the tag nucleic acids in the set of tag nucleic acids.

48. The recombinant cell of claim 47, wherein the tags further comprise a constant region, wherein the variable region does not cross hybridize with the constant region under stringent hybridization conditions.

49. The recombinant cell of claim 47, wherein the cell is selected from a library of genetically distinct recombinant cells.

50. The recombinant cell of claim 47, wherein the cell is a eukaryotic cell.

51. The recombinant cell of claim 47, wherein the cell is a prokaryotic cell.

52. The recombinant cell of claim 47, wherein the cell is a yeast cell.

53. A kit comprising an array of oligonucleotides, wherein

the array of oligonucleotide probes comprises a plurality of experimental oligonucleotide probe sets attached to a solid substrate;

each experimental oligonucleotide probe set in the array hybridizes to a different target nucleic acid under stringent hybridization conditions;

each oligonucleotide probe in the probe sets of the array comprises a variable region; and

the nucleic acid probes do not cross-hybridize in the array.

54. The kit of claim 53, wherein each oligonucleotide in the array further comprises a constant region, wherein the variable region does not cross hybridize with the constant region under stringent hybridization conditions.

55. The kit of claim 53, wherein the kit further comprises a plurality of tag nucleic acids complementary to the experimental oligonucleotide probes in the array.

56. The kit of claim 53, wherein the array further comprises control oligonucleotide probes.

57. The kit of claim 53, wherein the kit further comprises PCR reagents, a container and instructions.